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Appl. No. 10/668,778  
Amdt. dated October 29, 2007  
Amendment under 37 CFR 1.116 Expedited Procedure  
Examining Group 1639

**Amendments to the Claims:**

This listing of claims will replace all prior versions, and listings, of claims in the application:

**Listing of Claims:**

1. - 62. (Cancelled)

63. (Currently amended) A fragment complementation system, said system comprising:] a first oligopeptide sequence and a second oligopeptide sequence;

wherein said first oligopeptide sequence is a fusion protein comprised of and in the direction of translation, an N-terminal fragment of a Class A  $\beta$ -lactamase protein, not less than at least 25 amino acids in length, fused through a first break-point terminus to a first flexible polypeptide linker and a first interactor domain; and

wherein said second oligopeptide sequence is a fusion protein comprised of and in the direction of translation, a second interactor domain and a second flexible polypeptide linker fused through a second break-point terminus to a C-terminal fragment of a Class A  $\beta$ -lactamase protein, not less than at least 25 amino acids in length;

wherein said first and second break-point termini are ~~within 10 amino acids in either direction from a junction between 2 amino acid residues in, wherein said 2 amino acid residues are within~~ a solvent exposed loop between amino acid residues Thr 195 and Ala 202 ~~elements of secondary structure~~ and,

wherein upon binding of said first interactor domain with said second interactor domain, said N-terminal fragment and said C-terminal fragment ~~functionally~~ reconstitute to form a functional the Class A  $\beta$ -lactamase protein.

64. (Withdrawn- Previously presented) The fragment complementation system of claim 63, wherein said first oligopeptide and said second oligopeptide comprise a signal peptide that translocates said first oligopeptide and said second oligopeptide through the

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plasma membrane of a host cell in which said first oligopeptide and said second oligopeptide are expressed.

65. (Canceled)

66. (Currently amended) The fragment complementation system of claim 63, wherein said Class A  $\beta$ -lactamase protein comprises amino acids 26 to 288 of the following sequence:

His	Pro	Glu	Thr	Leu	Val	Lys	Val	Lys	Asp	Ala	Glu	Asp	Gln	Leu	Gly
26				30				35						40	
Ala	Arg	Val	Gly	Tyr	Ile	Glu	Leu	Asp	Leu	Asn	Ser	Gly	Lys	Ile	Leu
			45					50						55	
Glu	Ser	Phe	Arg	Pro	Glu	Glu	Arg	Phe	Pro	Met	Met	Ser	Thr	Phe	Lys
		60					65						70		
Val	Leu	Leu	Cys	Gly	Ala	Val	Leu	Ser	Arg	Ile	Asp	Ala	Gly	Gln	Glu
		75					80						85		
Gln	Leu	Gly	Arg	Arg	Ile	His	Tyr	Ser	Gln	Asn	Asp	Leu	Val	Glu	Tyr
90				95						100				105	
Ser	Pro	Val	Thr	Glu	Lys	His	Leu	Thr	Asp	Gly	Met	Thr	Val	Arg	Glu
				110					115					120	
Leu	Cys	Ser	Ala	Ala	Ile	Thr	Met	Ser	Asp	Asn	Thr	Ala	Ala	Asn	Leu
			125					130						135	
Leu	Leu	Thr	Thr	Ile	Gly	Gly	Pro	Lys	Glu	Leu	Thr	Ala	Phe	Ile	His
		140					145							150	
Asn	Met	Gly	Asp	His	Val	Thr	Arg	Leu	Asp	Arg	Trp	Glu	Pro	Glu	Leu
		155						160						165	
Asn	Glu	Ala	Ile	Pro	Asn	Asp	Glu	Arg	Asp	Thr	Thr	Met	Pro	Val	Ala
170				175						180				185	
Met	Ala	Thr	Thr	Leu	Arg	Lys	Leu	Leu	Thr	Gly	Glu	Leu	Leu	Thr	Leu

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	190	195	200
Ala Ser Arg Gln Gln Leu Ile Asp Trp Met Glu Ala Asp Lys Val Ala			
205	210	215	
Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala Gly Trp Phe Ile Ala Asp			
220	225	230	
Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile Ile Ala Ala Leu			
235	240	245	
Gly Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile Tyr Thr Thr Gly			
250	255	260	265
Ser Gln Ala Thr Met Asp Glu Arg Asn Arg Gln Ile Ala Glu Ile Gly			
270	275	280	
Ala Ser Leu Ile Lys His Trp			
285			

(SEQ ID NO:2);

wherein said ~~junction is~~ first and second break-point is between amino acid  
~~residues selected from the group consisting of P174 and N175, E197 Glu 197 and Leu 198 L198,~~  
~~K215 and V216, A227 and G228, and G253 and K254.~~

67. (Canceled).

68. (Withdrawn-Previously Presented) The fragment complementation system of claim 63, wherein said fragment complementation system further comprises a first peptide that enhances the functional reconstitution of said N-terminal fragment and said C-terminal fragment in comparison with the identical system without said first peptide, wherein said first peptide is 3-12 amino acids in length.

69. (Withdrawn-Previously Presented) The fragment complementation system of claim 68, wherein said first peptide is 3 amino acids in length.

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70. (Withdrawn-Previously Presented) The fragment complementation system of claim 69, wherein said first peptide is covalently bonded to the active site of a thioredoxin protein, wherein the sequence of said first peptide is GRE.

71. (Previously presented) The fragment complementation system of claim 63, wherein

said first polypeptide linker is 3-30 amino acids in length; and  
wherein said second polypeptide linker is 3-30 amino acids in length.

72. (Currently amended) The fragment complementation system of claim 71, wherein

~~said first oligopeptide further comprising~~ comprises a first complementation enhancement peptide fused between the N-terminal fragment of a the Class A  $\beta$ -lactamase protein and the first polypeptide linker; and

~~said second oligopeptide further comprises~~ a second complementation enhancement peptide fused between the C-terminal fragment of a the Class A  $\beta$ -lactamase protein and the second polypeptide linker.

73. (Previously Presented) The fragment complementation system of claim 72, wherein

the sequence of said first complementation enhancement peptide is selected from the group consisting of HSE, GRE, EKR, and NGR, and

the sequence of said second complementation enhancement peptide is selected from the group consisting of REQ, QGN, DGR, GRR and GNS.

74. (Currently amended) The fragment complementation system of claim 73, wherein

if the sequence of said first complementation enhancement peptide is HSE, and  
~~then~~ the sequence of said second complementation enhancement peptide is REQ;

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~~if the sequence of said first complementation enhancement peptide is NGR, then the sequence of said second complementation enhancement peptide is selected from the group consisting of REQ and GNS;~~

~~if the sequence of said first complementation enhancement peptide is GRE, then the sequence of said second complementation enhancement peptide is DGR; and~~

~~if the sequence of said first complementation enhancement peptide is EKR, then the sequence of said second complementation enhancement peptide is GRR.~~

75. (New) The fragment complementation system of claim 73, wherein the sequence of said first complementation enhancement peptide is NGR, and the sequence of said second complementation enhancement peptide is QGN or GNS.

76. (New) The fragment complementation system of claim 73, wherein the sequence of said first complementation enhancement peptide is GRE, and the sequence of said second complementation enhancement peptide is DGR.

77. (New) The fragment complementation system of claim 73, wherein the sequence of said first complementation enhancement peptide is EKR, and the sequence of said second complementation enhancement peptide is GRR.